



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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APPLICANTS: Hardin et al.
SERIAL NO.: 10/007,621
FILED: 12/03/01

§ ART UNIT NO.: 1645
§ EXAMINER: UNKNOWN
§ DOCKET NO.: 00007/02UTL

TITLE: Enzymatic Nucleic Acid Synthesis:
Compositions and Methods for Altering
Monomer Incorporation Fidelity

RECEIVED

FEB 06 2003

TECH CENTER 1600/2900

EV 192 402 080 US	CERTIFICATE OF MAIL BY EXPRESS MAIL	28 January 2003
Express Mail Number		Date of Deposit
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Assistant Commissioner of Patent		
BOX SEQUENCE		
Robert W. Strozier	Washington, D.C. 20231	28 January 2003
		Date of Signature

RESPONSE TO THE NOTICE TO COMPLY WITH SEQUENCE RULES

Dear Sir:

The Applicant hereby responds to the **Notice to Comply with Sequence Rules of 23 December 2002** and submits the following documents:

- (1) **Copy of Notice to Comply with Sequence Rules;**
- (2) **A Substitute Paper "Sequence Listing" and an identical "Sequence Listing" in computer readable, generated by the PatentIn 3.1 Software and check by Check 3.0; and a statement of identity of sequences.**
- (4) **Post Card.**

Respectfully submitted,

Robert W. Strozier, Reg. No. 34,024
Attorney for Applicants

Date: **28 January 2003**

Page 1



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BOX SEQUENCE		
Robert W. Strozier	Washington, D.C. 20231	28 January 2003
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STATEMENT REGARDING SUBSTITUTE PAPER COPY OF SEQUENCE
LISTING AND CRF COPY OF SEQUENCE LISTING

Dear Sir/Madam:

In response to a Notice to Comply with Sequence Rules, Applicant used the PatentIn 3.1 software for the United States Patent and Trademark Office to generate a hard copy and electronic copy of the sequence listing as required by the Notice.

Applicants' Attorney verifies that the paper and electronic listing are identical, both generated by PatentIn 3.1. Applicant has used the definitions of the sequences as set forth on Page 14 paragraph 66 (atgcctg) and Page 59 Table 1 for the remaining sequences.

Applicants' Attorney has attempted in good faith to respond to this notice; however, Applicants' Attorney must point out that at numerous parts of the specification, reference is made to specific enzymes and DNA molecules, without the actual sequences being included. Applicants did not include actual sequences because the actual sequences are not germane to this application. The application relates to functionalized dNTPs or other small molecules that increase base incorporation fidelity. The invention is not related to any specific nucleic

Page 1

Statement Regarding Substitute Paper Copy of Sequence Listing and crf Copy of Sequence Listing

Express Mail Label No.: EV 192 402 080 US

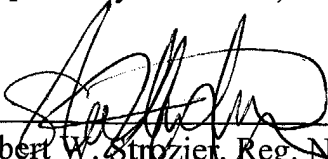
W:\Client Files\TUVW\VISIGEN\VisiGen02\UTL\Res to 11-22-02 Notice to Comply with Sequence Rules.wpd

ROBERT W. STROZIER, P.L.L.C.

acid sequence or peptide sequence.

Respectfully submitted,

Date: **28 January 2003**



Robert W. Strozier, Reg. No. 34,024
Attorney for Applicants

Page 2

Statement Regarding Substitute Paper Copy of Sequence Listing and crf Copy of Sequence Listing

Express Mail Label No.: EV 192 402 080 US

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ROBERT W. STROZIER, P.L.L.C.

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Commissioner for Patents
Washington, DC 20231
www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
10/007,621	12/03/2001	Susan H. Hardin	00007/02UTL

23873
ROBERT W STROZIER, PLLC
2925 BRIARPARK, SUITE 930
HOUSTON, TX 77042

CONFIRMATION NO. 9970

FORMALITIES LETTER



OC000000009149869

Date Mailed: 12/23/2002

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

RECEIVED

Filing Date Granted

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

*A copy of this notice **MUST** be returned with the reply.*

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 1 - ATTORNEY/APPLICANT COPY

DOCKETED

BY llm DATE 1/2/03
FOR ACTION ON FOLLOWING DAT.

llm 1/22/03

llm 2/13/03



UNITED STATES
PATENT AND
TRADEMARK OFFICE

Commissioner for Patents
Washington, DC 20231
www.uspto.gov

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10/007,621	12/03/2001	Susan H. Hardin	00007/02UTL

23873
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2925 BRIARPARK, SUITE 930
HOUSTON, TX 77042

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Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE



Visigen-02UTL.ST25
SEQUENCE LISTING

<110> Visigen Biotechnologies, Inc.

<120> Enzymatic Nucleic Acid Synthesis: Compositions and Methods for Altering Monomer Incorporation Fidelity

<130> 00007/02PCT

<140> PCT/US01/45819

<141> 2001-12-03

<150> 60/250,764

<151> 2000-12-01

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 7

<212> DNA

<213> Artificial

<220>

<223> The sequences listed here are artificially generated DNA sequences synthesized to test fidelity of monomer incorporation due to substitution at the gamma phosphate of the dNTPs.

<220>

<221> oligonucleotide

<222> (1)..(7)

<223> An example of an oligonucleotide discussed the in the definition section of the application.

<400> 1

atgcctg 7

<210> 2

<211> 19

<212> DNA

<213> Artificial

<220>

<223> This sequence is a primer strand for Taq DNA polymerase.

<220>

<221> primer_bind

<222> (1)..(19)

<223> Primer strand for Taq DNA polymerase

<400> 2

ggtactaagc ggccgcatg 19

<210> 3

<211> 20

<212> DNA

<213> Artificial

Visigen-02UTL.ST25

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a T residue at the end of the strand designated BOT-T 3'.

<220>
 <221> Template
 <222> (1)..(19)
 <223> Anti-sense to the primer sequence 2.

<400> 3
 ccatgattcg ccggcgctact 20

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a C residue at the end of the strand designated BOT-C 3'.

<220>
 <221> Template
 <222> (1)..(19)
 <223> Anti-sense to the primer sequence 2.

<400> 4
 ccatgattcg ccggcggtacc 20

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a G residue at the end of the strand designated BOT-G 3'.

<220>
 <221> Template
 <222> (1)..(19)
 <223> Anti-sense to the primer sequence 2.

<400> 5
 ccatgattcg ccggcggracg 20

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a A residue at the end of the strand designated

d BOT-A 3'.

<220>
 <221> Template
 <222> (1)..(19)
 <223> Anti-sense to the primer sequence 2.

<400> 6
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<210> 7
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a TAG residues at the end of the strand designed BOT-Sau 3'.

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 <221> Template
 <222> (1)..(19)
 <223> Anti-sense to the primer sequence 2.

<400> 7
 ccatgattcg ccggcgtacc tag 23

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a TC residues at the end of the strand designated BOT-TC 3'.

<220>
 <221> Template
 <222> (1)..(19)
 <223> Anti-sense to the primer sequence 2.

<400> 8
 ccatgattcg ccggcgtact c 21

<210> 9
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Template Strand - antisense to the primer strand of sequence 2 with the addition of a TTTC residues at the end of the strand designated BOT-3TC 3'.

<220>

<221> Template
<222> (1)..(19)
<223> Anti-sense to the primer sequence 2.

<400> 9
ccatgattcg ccggcgtact ttc

23